

16

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Vinik, Aaron
Pittenger, Gary
Rafaeloff, Ronit
Barlow, Scott

(ii) TITLE OF THE INVENTION: HIGH LEVEL EXPRESSION OF
INGAP

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Banner & Witcoff, Ltd.
(B) STREET: 1001 G Street, N.W.
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20001

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/741,096
(B) FILING DATE: 30-OCT-1996
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kagan, Sarah A
(B) REGISTRATION NUMBER: 32,145
(C) REFERENCE/DOCKET NUMBER: 0570.01435

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-508-9100
(B) TELEFAX: 202-508-9299
(C) TELEX: 97430 BMB UT

17

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGCAAGACA GGTACCATGA TGCTTCCCAT GACCCTCTGT AGGATGTCTT GGATGCTGCT 60
TTCCTGCCTG ATGTTCCITT CTTGGGTGGA AGGT 94

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGCGGATCC CGAAGAATCT CAAAAGAAAC T 31

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACCGGCTCG AGTGCTCTTC CTGAGTGAAT CC 32

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

CCGCGGATCC CGAAGAATCT CAAAAGAAAC TGCCTTCTTC ACGTATAACC TGTCCTCAAG      60
GCTCTGTAGC CTATGGGTCC TATTGCTATT CACTGATTTT GATACCACAG ACCTGGTCTA      120
ATGCAGAACT ATCCTGCCAG ATGCATTTCT CAGGACACCT GGCATTCTTT CTCAGTACTG      180
GTGAAATTAC CTTCGTGTCC TCCCTTGTGA AGAACAGTTT GACGGCCTAC CAGTACATCT      240
GGATTGGACT CCATGATCCC TCACATGGTA CACTACCCAA CGGAAGTGGG TGGAAGTGGG      300
GCAGTTCCAA TGTGCTGACC TTCTATAACT GGGAGAGGAA CCCCTCTATT GCTGCTGACC      360
GTGGTTATTG TGCAGTTTTG TCTCAGAAAT CAGGTTTTCA GAAGTGGAGA GATTTTAATT      420
GTGAAAATGA GCTTCCCTAT ATCTGCAAAT TCAAGGTCTA GGGCAGTTCT AATTTCAACA      480
GCTTGAAAAT ATTATGAAGC TCACATGGAC AAGGAAGCAA GTATGAGGAT TCACTCAGGA      540
AGAGCACTCG AGCCGGTC

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Met Leu Pro Met Thr Leu Cys Arg Met Ser Trp Met Leu Leu Ser
 1             5             10             15
Cys Leu Met Phe Leu Ser Trp Val Glu Gly
      20             25

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Met Leu Pro Met Thr Leu Cys Arg Met Ser Trp Met Leu Leu Ser
 1             5             10             15
Cys Leu Met Phe Leu Ser Trp Val Glu Gly Glu Glu Ser Gln Lys Lys
      20             25             30
Leu Pro Ser Ser Arg Ile Thr Cys Pro Gln Gly Ser Val Ala Tyr Gly
      35             40             45
Ser Tyr Cys Tyr Ser Leu Ile Leu Ile Pro Gln Thr Trp Ser Asn Ala
      50             55             60
Glu Leu Ser Cys Gln Met His Phe Ser Gly His Leu Ala Phe Leu Leu

```

19

65					70					75				80
Ser	Thr	Gly	Glu	Ile	Thr	Phe	Val	Ser	Ser	Leu	Val	Lys	Asn	Ser
					85				90				95	
Thr	Ala	Tyr	Gln	Tyr	Ile	Trp	Ile	Gly	Leu	His	Asp	Pro	Ser	His
					100			105					110	
Thr	Leu	Pro	Asn	Gly	Ser	Gly	Trp	Lys	Trp	Ser	Ser	Ser	Asn	Val
					115			120					125	
Thr	Phe	Tyr	Asn	Trp	Glu	Arg	Asn	Pro	Ser	Ile	Ala	Ala	Asp	Arg
					130			135					140	
Tyr	Cys	Ala	Val	Leu	Ser	Gln	Lys	Ser	Gly	Phe	Gln	Lys	Trp	Arg
					145			150					155	
Phe	Asn	Cys	Glu	Asn	Glu	Leu	Pro	Tyr	Ile	Cys	Lys	Phe	Lys	Val
					165			170					175	